FIGURE 1A – 1


1 M A L R R S M G R P G L P P L P L P P P P R L G L L L A A L A S
1 CCGCCGATGG CGCTGAGGCG GAGCATGGGG CGGCCGGGGC TCCCGCCGCT GCCGCTGCCG CCGCCACCGC GGCTCGGGCT GCTGCTGGCG GCTCTGGCTT
33 L L L P E S A A A G L K L M G A P V K L T V S Q G Q P V K L N C S
101 CTCTGCTGCT CCCGGAGTCC GCCGCCGCAG GTCTGAAGCT CATGGGAGCC CCGGTGAAGC TGACAGTGTC TCAGGGGCAG CCGGTGAAGC TCAACTGCAG
66 V E G M E E P D I Q W V K D G A V V Q N L D Q L Y I P V S E Q H W
201 TGTGGAGGGG ATGGAGGAGC CTGACATCCA GTGGGTGAAG GATGGGGCTG TGGTCCAGAA CTTGGACCAG TTGTACATCC CAGTCAGCGA GCAGCACTGG
99 I G F L S L K S V E R S D A G R Y W C Q V E D G G E T E I S Q P V W
301 ATCGGCTTCC TCAGCCTGAA GTCAGTGGAG CGCTCTGACG CCGGCCGGTA CTGGTGCCAG GTGGAGGATG GGGGTGAAAC CGAGATCTCC CAGCCAGTGT
133 L T V E G V P F F T V E P K D L A V P P N A P F Q L S C E A V G P
401 GGCTCACGGT AGAAGGTGTG CCATTTTTCA CAGTGGAGCC AAAAGATCTG GCAGTGCCAC CCAATGCCCC TTTCCAACTG TCTTGTGAGG CTGTGGGTCC
166 P E P V T I V W W R G T T K I G G P A P S P S V L N V T G V T Q S
501 CCCTGAACCT GTTACCATTG TCTGGTGGAG AGGAACTACG AAGATCGGGG GACCCGCTCC CTCTCCATCT GTTTTAAATG TAACAGGGGT GACCCAGAGC
199 T M F S C E A H N L K G L A S S R T A T V H L Q A L P A A P F N I T
601 ACCATGTTTT CCTGTGAAGC TCACAACCTA AAAGGCCTGG CCTCTTCTCG CACAGCCACT GTTCACCTTC AAGCACTGCC TGCAGCCCCC TTCAACATCA
233 V T K L S S S N A S V A W M P G A D G R A L L Q S C T V Q V T Q A
701 CCGTGACAAA GCTTTCCAGC AGCAACGCTA GTGTGGCCTG GATGCCAGGT GCTGATGGCC GAGCTCTGCT ACAGTCCTGT ACAGTTCAGG TGACACAGGC
266 P G G W E V L A V V V P V P P F T C L L R D L V P A T N Y S L R V
801 CCCAGGAGGC TGGGAAGTCC TGGCTGTTGT GGTCCCTGTG CCCCCCTTTA CCTGCCTGCT CCGGGACCTG GTGCCTGCCA CCAACTACAG CCTCAGGGTG
299 R C A N A L G P S P Y A D W V P F Q T K G L A P A S A P Q N L H A I
901 CGCTGTGCCA ATGCCTTGGG GCCCTCTCCC TATGCTGACT GGGTGCCCTT TCAGACCAAG GGTCTAGCCC CAGCCAGCGC TCCCCAAAAC CTCCATGCCA
333 R T D S G L I L E W E E V I P E A P L E G P L G P Y K L S W V Q D
1001 TCCGCACAGA TTCAGGCCTC ATCTTGGAGT GGGAAGAAGT GATCCCCGAG GCCCCTTTGG AAGGCCCCCT GGGACCCTAC AAACTGTCCT GGGTTCAAGA
366 N G T Q D E L T V E G T R A N L T G W D P Q K D L I V R V C V S N
1101 CAATGGAACC CAGGATGAGC TGACAGTGGA GGGGACCAGG GCCAATTTGA CAGGCTGGGA TCCCCAAAAG GACCTGATCG TACGTGTGTG CGTCTCCAAT
399 A V G C G P W S Q P L V V S S H D R A G Q Q G P P H S R T S W V P V
1201 GCAGTTGGCT GTGGACCCTG GAGTCAGCCA CTGGTGGTCT CTTCTCATGA CCGTGCAGGC CAGCAGGGCC CTCCTCACAG CCGCACATCC TGGGTACCTG
433 V L G V L T A L V T A A A L A L I L L R K R R K E T R F G Q A F D
1301 TGGTCCTTGG TGTGCTAACG GCCCTGGTGA CGGCTGCTGC CCTGGCCCTC ATCCTGCTTC GAAAGAGACG GAAAGAGACG CGGTTTGGGC AAGCCTTTGA

FIGURE 1A-2

```
 466 S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L
1401 CAGTGTCATG GCCCGGGGAG AGCCAGCCGT TCACTTCCGG GCAGCCCGGT CCTTCAATCG AGAAAGGCCC GAGCGCATCG AGGCCACATT GGACAGCTTG

 499 G I S D E L K E K L E D V L I P E Q Q F T L G R M L G K G E F G S V
1501 GGCATCAGCG ATGAACTAAA GGAAAAACTG GAGGATGTGC TCATCCCAGA GCAGCAGTTC ACCCTGGGCC GGATGTTGGG CAAAGGAGAG TTTGGTTCAG

 533 R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E F
1601 TGCGGGAGGC CCAGCTGAAG CAAGAGGATG GCTCCTTTGT GAAAGTGGCT GTGAAGATGC TGAAAGCTGA CATCATTGCC TCAAGCGACA TTGAAGAGTT

 566 L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I
1701 CCTCAGGGAA GCAGCTTGCA TGAAGGAGTT TGACCATCCA CACGTGGCCA AACTTGTTGG GGTAAGCCTC CGGAGCAGGG CTAAAGGCCG TCTCCCCATC

 599 P M V I L P F M K H G D L H A F L L A S R I G E N P F N L P L Q T L
1801 CCCATGGTCA TCTTGCCCTT CATGAAGCAT GGGGACCTGC ATGCCTTCCT GCTCGCCTCC CGGATTGGGG AGAACCCCTT TAACCTACCC CTCCAGACCC

 633 I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A E
1901 TGATCCGGTT CATGGTGGAC ATTGCCTGCG GCATGGAGTA CCTGAGCTCT CGGAACTTCA TCCACCGAGA CCTGGCTGCT CGGAATTGCA TGCTGGCAGA

 666 D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K W
2001 GGACATGACA GTGTGTGTGG CTGACTTCGG ACTCTCCCGG AAGATCTACA GTGGGGACTA CTATCGTCAA GGCTGTGCCT CCAAACTGCC TGTCAAGTGG

 699 L A L E S L A D N L Y T V Q S D V W A F G V T M W E I M T R G Q T P
2101 CTGGCCCTGG AGAGCCTGGC CGACAACCTG TATACTGTGC AGAGTGACGT GTGGGCGTTC GGGGTGACCA TGTGGGAGAT CATGACACGT GGGCAGACGC

 733 Y A G I E N A E I Y N Y L I G G N R L K Q P P E C M E D V Y D L M
2201 CATATGCTGG CATCGAAAAC GCTGAGATTT ACAACTACCT CATTGGCGGG AACCGCCTGA AACAGCCTCC GGAGTGTATG GAGGACGTGT ATGATCTCAT

 766 Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A
2301 GTACCAGTGC TGGAGTGCTG ACCCCAAGCA GCGCCCGAGC TTTACTTGTC TGCGAATGGA ACTGGAGAAC ATCTTGGGCC AGCTGTCTGT GCTATCTGCC

 799 S Q D P L Y I N I E R A E E P T A G G S L E L P G R D Q P Y S G A G
2401 AGCCAGGACC CCTTATACAT CAACATCGAG AGAGCTGAGG AGCCCACTGC GGGAGGCAGC CTGGAGCTAC CTGGCAGGGA TCAGCCCTAC AGTGGGGCTG

 833 D G S G M G A V G G T P S D C R Y I L T P G G L A E Q P G Q A E H
2501 GGGATGGCAG TGGCATGGGG GCAGTGGGTG GCACTCCCAG TGACTGTCGG TACATACTCA CCCCCGGAGG GCTGGCTGAG CAGCCAGGGC AGGCAGAGCA

 866 Q P E S P L N E T Q R L L L L Q Q G L L P H S S C O
2601 CCAGCCAGAG AGTCCCCTCA ATGAGACACA GAGGCTTTTG CTGCTGCAGC AAGGGCTACT GCCACACAGT AGCTGTTAGC CCACAGGCAG AGGGCATCGG

2701 GGCCATTTGG CCGGCTCTGG TGGCCACTGA GCTGGCTGAC TAAGCCCCGT CTGACCCCAG CCCAGACAGC AAGGTGTGGA GGCTCCTGTG GTAGTCCTCC

2801 CAAGCTGTGC TGGGAAGCCC GGACTGACCA AATCACCCAA TCCCAGTTCT TCCTGCAACC ACTCTGTGGC CAGCCTGGCA TCAGTTTAGG CCTTGGCTTG
```

FIGURE 1A-3

2901 ATGGAAGTGG GCCAGTCCTG GTTGTCTGAA CCCAGGCAGC TGGCAGGAGT GGGGTGGTTA TGTTTCCATG GTTACCATGG GTGTGGATGG CAGTGTGGGG

3001 AGGGCAGGTC CAGCTCTGTG GGCCCTACCC TCCTGCTGAG CTGCCCCTGC TGCTTAAGTG CATGCATTGA GCTGCCTCCA GCCTGGTGGC CCAGCTATTA

3101 CCACACTTGG GGTTTAAATA TCCAGGTGTG CCCCTCCAAG TCACAAAGAG ATGTCCTTGT AATATTCCCT TTTAGGTGAG GGTTGGTAAG GGGTTGGTAT

3201 CTCAGGTCTG AATCTTCACC ATCTTTCTGA TTCCGCACCC TGCCTACGCC AGGAGAAGTT GAGGGGAGCA TGCTTCCCTG CAGCTGACCG GGTCACACAA

3301 AGGCATGCTG GAGTACCCAG CCTATCAGGT GCCCCTCTTC CAAAGGCAGC GTGCCGAGCC AGCAAGAGGA AGGGGTGCTG TGAGGCTTGC CCAGGAGCAA

3401 GTGAGGCCGG AGAGGAGTTC AGGAACCCTT CTCCATACCC ACAATCTGAG CACGCTACCA AATCTCAAAA TATCCTAAGA CTAACAAAGG CAGCTGTGTC

3501 TGAGCCCAAC CCTTCTAAAC GGTGACCTTT AGTGCCAACT TCCCCTCTAA CTGGACAGCC TCTTCTGTCC CAAGTCTCCA GAGAGAAATC AGGCCTGATG

3601 AGGGGGAATT C

FIGURE 1B-1

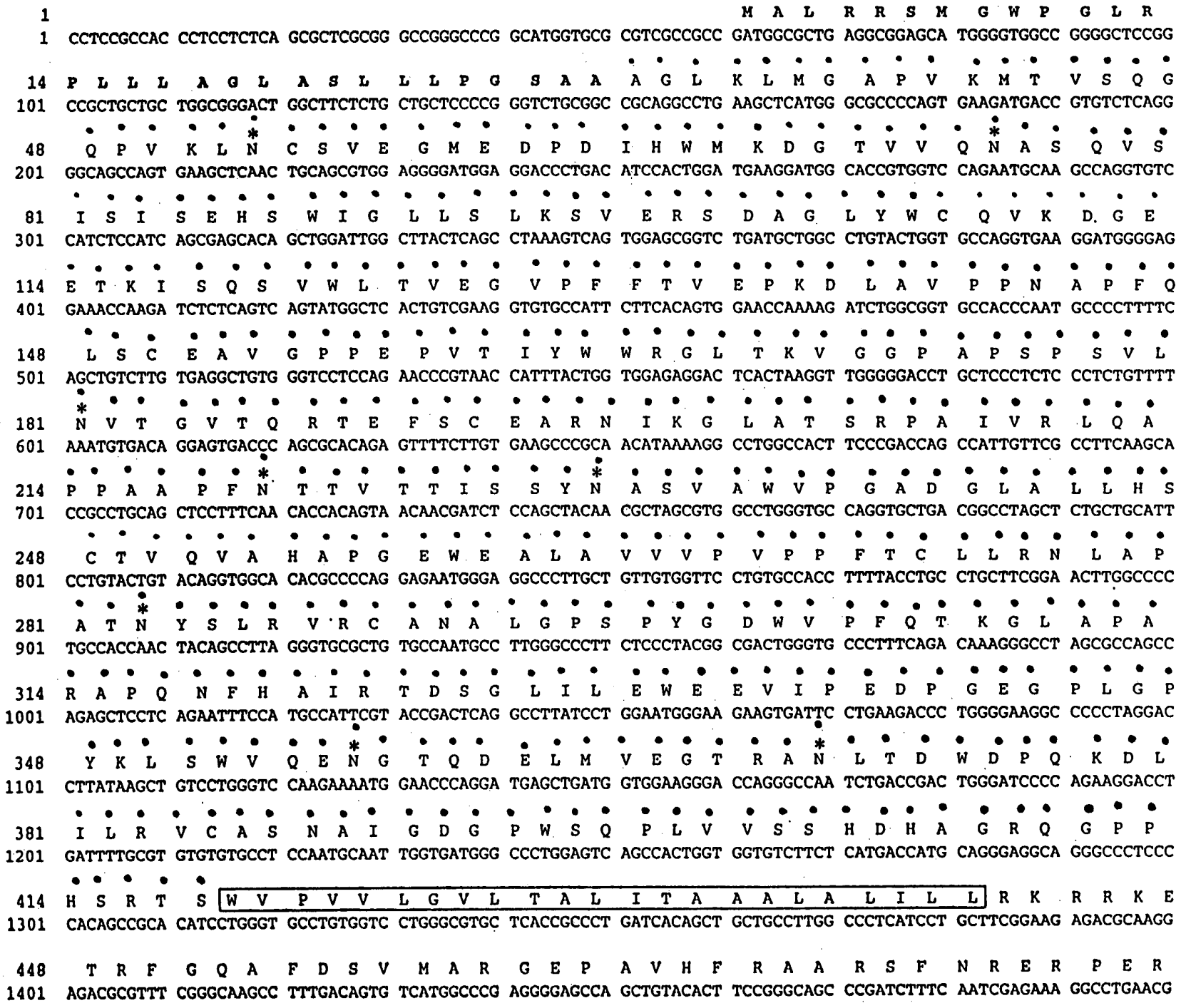
1 M A L R R S M G W P G L R
1 CCTCCGCCAC CCTCCTCTCA GCGCTCGCGG GCCGGGCCCG GCATGGTGCG CGTCGCCGCC GATGGCGCTG AGGCGGAGCA TGGGGTGGCC GGGGCTCCGG
14 P L L L A G L A S L L L P G S A A A G L K L M G A P V K M T V S Q G
101 CCGCTGCTGC TGGCGGGACT GGCTTCTCTG CTGCTCCCCG GGTCTGCGGC CGCAGGCCTG AAGCTCATGG GCGCCCCAGT GAAGATGACC GTGTCTCAGG
48 Q P V K L N C S V E G M E D P D I H W M K D G T V V Q N A S Q V S
201 GGCAGCCAGT GAAGCTCAAC TGCAGCGTGG AGGGGATGGA GGACCCTGAC ATCCACTGGA TGAAGGATGG CACCGTGGTC CAGAATGCAA GCCAGGTGTC
81 I S I S E H S W I G L L S L K S V E R S D A G L Y W C Q V K D G E
301 CATCTCCATC AGCGAGCACA GCTGGATTGG CTTACTCAGC CTAAAGTCAG TGGAGCGGTC TGATGCTGGC CTGTACTGGT GCCAGGTGAA GGATGGGGAG
114 E T K I S Q S V W L T V E G V P F F T V E P K D L A V P P N A P F Q
401 GAAACCAAGA TCTCTCAGTC AGTATGGCTC ACTGTCGAAG GTGTGCCATT CTTCACAGTG GAACCAAAAG ATCTGGCGGT GCCACCCAAT GCCCCTTTTC
148 L S C E A V G P P E P V T I Y W W R G L T K V G G P A P S P S V L
501 AGCTGTCTTG TGAGGCTGTG GGTCCTCCAG AACCCGTAAC CATTTACTGG TGGAGAGGAC TCACTAAGGT TGGGGGACCT GCTCCCTCTC CCTCTGTTTT
181 N V T G V T Q R T E F S C E A R N I K G L A T S R P A I V R L Q A
601 AAATGTGACA GGAGTGACCC AGCGCACAGA GTTTTCTTGT GAAGCCCGCA ACATAAAAGG CCTGGCCACT TCCCGACCAG CCATTGTTCG CCTTCAAGCA
214 P P A A P F N T T V T T I S S Y N A S V A W V P G A D G L A L L H S
701 CCGCCTGCAG CTCCTTTCAA CACCACAGTA ACAACGATCT CCAGCTACAA CGCTAGCGTG GCCTGGGTGC CAGGTGCTGA CGGCCTAGCT CTGCTGCATT
248 C T V Q V A H A P G E W E A L A V V V P V P P F T C L L R N L A P
801 CCTGTACTGT ACAGGTGGCA CACGCCCCAG GAGAATGGGA GGCCCTTGCT GTTGTGGTTC CTGTGCCACC TTTTACCTGC CTGCTTCGGA ACTTGGCCCC
281 A T N Y S L R V R C A N A L G P S P Y G D W V P F Q T K G L A P A
901 TGCCACCAAC TACAGCCTTA GGGTGCGCTG TGCCAATGCC TTGGGCCCTT CTCCCTACGG CGACTGGGTG CCCTTTCAGA CAAAGGGCCT AGCGCCAGCC
314 R A P Q N F H A I R T D S G L I L E W E E V I P E D P G E G P L G P
1001 AGAGCTCCTC AGAATTTCCA TGCCATTCGT ACCGACTCAG GCCTTATCCT GGAATGGGAA GAAGTGATTC CTGAAGACCC TGGGGAAGGC CCCCTAGGAC
348 Y K L S W V Q E N G T Q D E L M V E G T R A N L T D W D P Q K D L
1101 CTTATAAGCT GTCCTGGGTC CAAGAAAATG GAACCCAGGA TGAGCTGATG GTGGAAGGGA CCAGGGCCAA TCTGACCGAC TGGGATCCCC AGAAGGACCT
381 I L R V C A S N A I G D G P W S Q P L V V S S H D H A G R Q G P P
1201 GATTTTGCGT GTGTGTGCCT CCAATGCAAT TGGTGATGGG CCCTGGAGTC AGCCACTGGT GGTGTCTTCT CATGACCATG CAGGGAGGCA GGGCCCTCCC
414 H S R T S W V P V V L G V L T A L I T A A A L A L I L L R K R R K E
1301 CACAGCCGCA CATCCTGGGT GCCTGTGGTC CTGGGCGTGC TCACCGCCCT GATCACAGCT GCTGCCTTGG CCCTCATCCT GCTTCGGAAG AGACGCAAGG
448 T R F G Q A F D S V M A R G E P A V H F R A A R S F N R E R P E R
1401 AGACGCGTTT CGGGCAAGCC TTTGACAGTG TCATGGCCCG AGGGGAGCCA GCTGTACACT TCCGGGCAGC CCGATCTTTC AATCGAGAAA GGCCTGAACG

FIGURE 1B-2

```
481   I  E  A  T  L  D  S  L  G  I  S  D  E  L  K  E  K  L  E  D  V  L  I  P  E  Q  Q  F  T  L  G  R  M
1501  CATTGAGGCC ACATTGGATA GCCTGGGCAT CAGCGATGAA TTGAAGGAAA AGCTGGAGGA TGTCCTCATT CCAGAGCAGC AGTTCACCCT CGGTCGGATG

514   L  G  K  G  E  F  G  S  V  R  E  A  Q  L  K  Q  E  D  G  S  F  V  K  V  A  V  K  M  L  K  A  D  I  I
1601  TTGGGCAAAG GAGAGTTTGG ATCAGTGCGG GAAGCCCAGC TAAAGCAGGA AGATGGCTCC TTCGTGAAAG TGGCAGTGAA GATGCTGAAA GCTGACATCA

548   A  S  S  D  I  E  E  F  L  R  E  A  A  C  M  K  E  F  D  H  P  H  V  A  K  L  V  G  V  S  L  R  S
1701  TTGCCTCAAG CGACATAGAA GTGTTCCTCC GGGAAGCAGC TTGCATGAAG GAGTTTGACC ATCCACACGT GGCCAAGCTT GTTGGGGTGA GCCTCCGGAG

581   R  A  K  G  R  L  P  I  P  M  V  I  L  P  F  M  K  H  G  D  L  H  A  F  L  L  A  S  R  I  G  E  N
1801  CAGGGCTAAA GGTCGTCTCC CCATTCCCAT GGTCATCCTG CCCTTCATGA AACATGGAGA CTTGCACGCC TTTCTGCTCG CCTCCCGAAT CGGGGAGAAC

614   P  F  N  L  P  L  Q  T  L  V  R  F  M  V  D  I  A  C  G  M  E  Y  L  S  S  R  N  F  I  H  R  D  L  A
1901  CCTTTTAACC TGCCCCTGCA GACCCTGGTC CGGTTCATGG TGGACATTGC CTGTGGCATG GAGTACCTGA GCTCCCGGAA CTTCATCCAC CGAGACCTAG

648   A  R  N  C  M  L  A  E  D  M  T  V  C  V  A  D  F  G  L  S  R  K  I  Y  S  G  D  Y  Y  R  Q  G  C
2001  CAGCTCGGAA TTGCATGCTG GCCGAGGACA TGACAGTGTG TGTGGCTGAT TTTGGACTCT CTCGGAAAAT CTATAGCGGG GACTATTATC GTCAGGGCTG

681   A  S  K  L  P  V  K  W  L  A  L  E  S  L  A  D  N  L  Y  T  V  H  S  D  V  W  A  F  G  V  T  M  W
2101  TGCCTCCAAA TTGCCCGTCA AGTGGCTGGC CCTGGAGAGC TTGGCTGACA ACTTGTATAC TGTACACAGT GATGTGTGGG CCTTCGGGGT GACCATGTGG

714   E  I  M  T  R  G  Q  T  P  Y  A  G  I  E  N  A  E  I  Y  N  Y  L  I  G  G  N  R  L  K  Q  P  P  E  C
2201  GAGATCATGA CTCGTGGGCA GACGCCATAT GCTGGCATTG AAAATGCTGA GATTTACAAC TACCTCATCG GCGGGAACCG CCTGAAGCAG CCTCCGGAGT

748   M  E  E  V  Y  D  L  M  Y  Q  C  W  S  A  D  P  K  Q  R  P  S  F  T  C  L  R  M  E  L  E  N  I  L
2301  GCATGGAGGA AGTGTATGAT CTCATGTACC AGTGCTGGAG CGCCGACCCC AAGCAGCGCC CAAGCTTCAC GTGTCTGCGA ATGGAACTGG AGAACATTCT

781   G  H  L  S  V  L  S  T  S  Q  D  P  L  Y  I  N  I  E  R  A  E  Q  P  T  E  S  G  S  P  E  L  H  C
2401  GGGCCACCTG TCTGTGCTGT CCACCAGCCA GGACCCCTTG TACATCAACA TTGAGAGAGC TGAGCAGCCT ACTGAGAGTG GCAGCCCTGA GCTGCACTGT

814   G  E  R  S  S  S  E  A  G  D  G  S  G  V  G  A  V  G  G  I  P  S  D  S  R  Y  I  F  S  P  G  G  L  S
2501  GGAGAGCGAT CCAGCAGCGA GGCAGGGGAC GGCAGTGGCG TGGGGGCAGT AGGTGGCATC CCCAGTGACT CTCGGTACAT CTTCAGCCCC GGAGGGCTAT

848   E  S  P  G  Q  L  E  Q  Q  P  E  S  P  L  N  E  N  Q  R  L  L  L  L  Q  Q  G  L  L  P  H  S  S  C
2601  CCGAGTCACC AGGGCAGCTG GAGCAGCAGC CAGAAAGCCC CCTCAATGAG AACCAGAGGC TGTTGTTGCT GCAGCAAGGG CTACTGCCTC ACAGTAGCTG

881   O
2701  TTAACCCTCA GGCAGAGGAA AGTTGGGGCC CCTGGCTCTG CTGACCGCTG CGCTGCCTGA CTAGGCCCAG TCTGATCACA GCCCAGGCAG CAAGGTATGG

2801  AGGCTCCTGT GGTAGCCCTC CCAAGCTGTG TGGCGCCTGG ACGGACCAAA TTGCCCAATC CCAGTTCTTC CTGCAGCCGC TCTGGCCAGC CTGGCATCAG

2901  TTCAGGCCTT GGCTTAGAGG AGGTGAGCCA GAGCTGGTTG CCTGAATGCA GGCAGCTGGC AGGAGGGGAG GGTGGCTATG TTTCCATGGG TACCATGGGT

3001  GTGGATGGCA GTAAGGGAGG GTAGCAACAG CCTGTGGGCC CCTACCCTCC TGGCTGAGCT GCTCCTACTT TAGTGCATGC TTGGAGCCGC CTGCAGCCTG

3101  GAACTCAGCA CTGCCCACCA CACTTGGGCC GAAATGCCAG GTTTGCCCCT CTTAAGTCAC AAAGAGATGT CCATGTATTG TTCCCTTTTA GGTGATGATT
```

FIGURE 1B-3

```
3201  AGGAAGGGAT TGGCACACTT GGGTCCCTAA GCCCTATGGC AGGAAATGGT GGGATATTCT CAGGTCTGAA TCCTCATCAT CTTCCTGATT CCCCACCCTG

3301  CAAAGGCCTG GAACTGGCTG TGGGGCTCTG ACGCATGCTG AAGGACAAAA GGTTACAGAG ATCCGACTTC AAAAGGCAGG GTCTGAGTCT GGCAGGTGGA

3401  GAGGTGCTAA GGGGCTGGCC CAGGAGTCAG GCATTTCAGG ACCCCTCCAA GCTTCTACAG TCTGTCTGAG CATGCTACCA AGCCCCCAGA TACCCCAAAA

3501  CTAACAGAGG CAGTTTTGTC TGAGCCCAGC CCTCCCACAT GATGACCCTT AGGTCTACCC TCCTCTCTAA ATGGACATCC TCGTTTGTCC CAAGTCTCCA

3601  GAGAGACTAC TGATGGCTGA TGTGGGTAAG AAAAGTTCCA GGAACCAGGG CTGGGGTGGA ACCAGGGCTG GGGTCGAGGC AGGCTCTTGG GCAGGCTCTT

3701  GCTGTTAGGA ACATTTCTAA GCTATTAAGT TGCTGTTTCA AAACAAATAA AATTGAAACA TAAAGAATCA AAAAAAAAAA AAAAA
```

FIGURE 2 -1

```
  1 GAATTCTCGA GTCGACGTTG GACTTGAAGG AATGCCAAGA GATGCTGCCC

 51 CCACCCCCTT AGGCCCGAGG GATCAGGAGC TATGGGACCA GAGGCCCTGT
  1                                   MetGlyPro GluAlaLeuSer
                                                      ******

101 CATCTTTACT GCTGCTGCTC TTGGTGGCAA GTGGAGATGC TGACATGAAG
  8   SerLeuLe uLeuLeuLeu LeuValAlaS erGlyAspAl aAspMetLys
      ******** ********** ********** *****

151 GGACATTTTG ATCCTGCCAA GTGCCGCTAT GCCCTGGGCA TGCAGGACCG
 24 GlyHisPheA spProAlaLy sCysArgTyr AlaLeuGlyM etGlnAspArg

201 GACCATCCCA GACAGTGACA TCTCTGCTTC CAGCTCCTGG TCAGATTCCA
 41  ThrIlePro AspSerAspI leSerAlaSe rSerSerTrp SerAspSerThr

251 CTGCCGCCCG CCACAGCAGG TTGGAGAGCA GTGACGGGGA TGGGGCCTGG
 58   AlaAlaAr gHisSerArg LeuGluSerS erAspGlyAs pGlyAlaTrp

301 TGCCCCGCAG GGTCGGTGTT TCCCAAGGAG GAGGAGTACT TGCAGGTGGA
 74 CysProAlaG lySerValPh eProLysGlu GluGluTyrL euGlnValAsp

351 TCTACAACGA CTGCACCTGG TGGCTCTGGT GGGCACCCAG GGACGGCATG
 91  LeuGlnArg LeuHisLeuV alAlaLeuVa lGlyThrGln GlyArgHisAla

401 CCGGGGGCCT GGGCAAGGAG TTCTCCCGGA GCTACCGGCT GCGTTACTCC
108   GlyGlyLe uGlyLysGlu PheSerArgS erTyrArgLe uArgTyrSer

451 CGGGATGGTC GCCGCTGGAT GGGCTGGAAG GACCGCTGGG GTCAGGAGGT
124 ArgAspGlyA rgArgTrpMe tGlyTrpLys AspArgTrpG lyGlnGluVal

501 GATCTCAGGC AATGAGGACC CTGAGGGAGT GGTGCTGAAG GACCTTGGGC
141  IleSerGly AsnGluAspP roGluGlyVa lValLeuLys AspLeuGlyPro

551 CCCCCATGGT TGCCCGACTG GTTCGCTTCT ACCCCCGGGC TGACCGGGTC
158   ProMetVa lAlaArgLeu ValArgPheT yrProArgAl aAspArgVal

601 ATGAGCGTCT GTCTGCGGGT AGAGCTCTAT GGCTGCCTCT GGAGGGATGG
174 MetSerValC ysLeuArgVa lGluLeuTyr GlyCysLeuT rpArgAspGly

651 ACTCCTGTCT TACACCGCCC CTGTGGGGCA GACAATGTAT TTATCTGAGG
191  LeuLeuSer TyrThrAlaP roValGlyGl nThrMetTyr LeuSerGluAla

701 CCGTGTACCT CAACGACTCC ACCTATGACG GACATACCGT GGGCGGACTG
208   ValTyrLe uAsnAspSer ThrTyrAspG lyHisThrVa lGlyGlyLeu

751 CAGTATGGGG GTCTGGGCCA GCTGGCAGAT GGTGTGGTGG GGCTGGATGA
224 GlnTyrGlyG lyLeuGlyGl nLeuAlaAsp GlyValValG lyLeuAspAsp

801 CTTTAGGAAG AGTCAGGAGC TGCGGGTCTG GCCAGGCTAT GACTATGTGG
241  PheArgLys SerGlnGluL euArgValTr pProGlyTyr AspTyrValGly

851 GATGGAGCAA CCACAGCTTC TCCAGTGGCT ATGTGGAGAT GGAGTTTGAG
258   TrpSerAs nHisSerPhe SerSerGlyT yrValGluMe tGluPheGlu
```

FIGURE 2-2

```
 901 TTTGACCGGC TGAGGGCCTT CCAGGCTATG CAGGTCCACT GTAACAACAT
 274 PheAspArgL euArgAlaPh eGlnAlaMet GlnValHisC ysAsnAsnMet

 951 GCACACGCTG GGAGCCCGTC TGCCTGGCGG GGTGGAATGT CGCTTCCGGC
 291  HisThrLeu GlyAlaArgL euProGlyGl yValGluCys ArgPheArgArg

1001 GTGGCCCTGC CATGGCCTGG GAGGGGGAGC CCATGCGCCA CAACCTAGGG
 308   GlyProAl aMetAlaTrp GluGlyGluP roMetArgHi sAsnLeuGly

1051 GGCAACCTGG GGGACCCCAG AGCCCGGGCT GTCTCAGTGC CCCTTGGCGG
 324 GlyAsnLeuG lyAspProAr gAlaArgAla ValSerValP roLeuGlyGly

1101 CCGTGTGGCT CGCTTTCTGC AGTGCCGCTT CCTCTTTGCG GGGCCCTGGT
 341  ArgValAla ArgPheLeuG lnCysArgPh eLeuPheAla GlyProTrpLeu

1151 TACTCTTCAG CGAAATCTCC TTCATCTCTG ATGTGGTGAA CAATTCCTCT
 358   LeuPheSe rGluIleSer PheIleSerA spValValAs nAsnSerSer

1201 CCGGCACTGG GAGGCACCTT CCCGCCAGCC CCCTGGTGGC CGCCTGGCCC
 374 ProAlaLeuG lyGlyThrPh eProProAla ProTrpTrpP roProGlyPro

1251 ACCTCCCACC AACTTCAGCA GCTTGGAGCT GGAGCCCAGA GGCCAGCAGC
 391  ProProThr AsnPheSerS erLeuGluLe uGluProArg GlyGlnGlnPro

1301 CCGTGGCCAA GCCCGAGGGG AGCCCGACCG CCATCCTCAT CGGCTGCCTG
 408   ValAlaLy sProGluGly SerProThrA laIleLeuIl eGlyCysLeu

1351 GTGGCCATCA TCCTGCTCCT GCTGCTCATC ATTGCCCTCA TGCTCTGGCG
 424 ValAlaIleI leLeuLeuLe uLeuLeuIle IleAlaLeuM etLeuTrpArg

1401 GCTGCACTGG CGCAGGCTCC TCAGCAAGGC TGAACGGAGG GTGTTGGAAG
 441  LeuHisTrp ArgArgLeuL euSerLysAl aGluArgArg ValLeuGluGlu

1451 AGGAGCTGAC GGTTCACCTC TCTGTCCCTG GGGACACTAT CCTCATCAAC
 458   GluLeuTh rValHisLeu SerValProG lyAspThrIl eLeuIleAsn

1501 AACCGCCCAG GTCCTAGAGA GCCACCCCCG TACCAGGAGC CCCGGCCTCG
 474 AsnArgProG lyProArgGl uProProPro TyrGlnGluP roArgProArg

1551 TGGGAATCCG CCCCACTCCG CTCCCTGTGT CCCCAATGGC TCTGCGTTGC
 491  GlyAsnPro ProHisSerA laProCysVa lProAsnGly SerAlaLeuLeu

1601 TGCTCTCCAA TCCAGCCTAC CGCCTCCTTC TGGCCACTTA CGCCCGTCCC
 508   LeuSerAs nProAlaTyr ArgLeuLeuL euAlaThrTy rAlaArgPro

1651 CCTCGAGGCC CGGGCCCCCC CACACCCGCC TGGGCCAAAC CCACCAACAC
 524 ProArgGlyP roGlyProPr oThrProAla TrpAlaLysP roThrAsnThr

1701 CCAGGCCTAC AGTGGGGACT ATATGGAGCC TGAGAAGCCA GGCGCCCCGC
 541  GlnAlaTyr SerGlyAspT yrMetGluPr oGluLysPro GlyAlaProLeu

1751 TTCTGCCCCC ACCTCCCCAG AACAGCGTCC CCCATTATGC CGAGGCTGAC
 558   LeuProPr oProProGln AsnSerValP roHisTyrAl aGluAlaAsp
```

FIGURE 2-3

```
1801 ATTGTTACCC TGCAGGGCGT CACCGGGGGC AACACCTATG CTGTGCCTGC
 574 IleValThrL euGlnGlyVa lThrGlyGly AsnThrTyrA laValProAla

1851 ACTGCCCCCA GGGGCAGTCG GGGATGGGCC CCCCAGAGTG GATTTCCCTC
 591  LeuProPro GlyAlaValG lyAspGlyPr oProArgVal AspPheProArg

1901 GATCTCGACT CCGCTTCAAG GAGAAGCTTG GCGAGGGCCA GTTTGGGGAG
 608   SerArgLe uArgPheLys GluLysLeuG lyGluGlyGl nPheGlyGlu
           << <                    .  .........  .......

1951 GTGCACCTGT GTGAGGTCGA CAGCCCTCAA GATCTGGTCA GTCTTGATTT
 624 ValHisLeuC ysGluValAs pSerProGln AspLeuValS erLeuAspPhe

2001 CCCCCTTAAT GTGCGTAAGG GACACCCTTT GCTGGTAGCT GTCAAGATCT
 641  ProLeuAsn ValArgLysG lyHisProLe uLeuValAla ValLysIleLeu

2051 TACGGCCAGA TGCCACCAAG AATGCCAGGA ATGATTTCCT GAAAGAGGTG
 658   ArgProAs pAlaThrLys AsnAlaArgA snAspPheLe uLysGluVal

2101 AAGATCATGT CGAGGCTCAA GGACCCAAAC ATCATTCGGC TGCTGGGCGT
 674 LysIleMetS erArgLeuLy sAspProAsn IleIleArgL euLeuGlyVal

2151 GTGTGTGCAG GACGACCCCC TCTGCATGAT TACTGACTAC ATGGAGAACG
 691  CysValGln AspAspProL euCysMetIl eThrAspTyr MetGluAsnGly

2201 GCGACCTCAA CCAGTTCCTC AGTGCCCACC AGCTGGAGGA CAAGGCAGCC
 708   AspLeuAs nGlnPheLeu SerAlaHisG lnLeuGluAs pLysAlaAla

2251 GAGGGGGCCC CTGGGGACGG GCAGGCTGCG CAGGGGCCCA CCATCAGCTA
 724 GluGlyAlaP roGlyAspGl yGlnAlaAla GlnGlyProT hrIleSerTyr

2301 CCCAATGCTG CTGCATGTGG CAGCCCAGAT CGCCTCCGGC ATGCGCTATC
 741  ProMetLeu LeuHisValA laAlaGlnIl eAlaSerGly MetArgTyrLeu

2351 TGGCCACACT CAACTTTGTA CATCGGGACC TGGCCACGCG GAACTGCCTA
 758   AlaThrLe uAsnPheVal HisArgAspL euAlaThrAr gAsnCysLeu

2401 GTTGGGGAAA ATTTCACCAT CAAAATCGCA GACTTTGGCA TGAGCCGGAA
 774 ValGlyGluA snPheThrIl eLysIleAla AspPheGlyM etSerArgAsn

2451 CCTCTATGCT GGGGACTATT ACCGTGTGCA GGGCCGGGCA GTGCTGCCCA
 791  LeuTyrAla GlyAspTyrT yrArgValGl nGlyArgAla ValLeuProIle

2501 TCCGCTGGAT GGCCTGGGAG TGCATCCTCA TGGGGAAGTT CACGACTGCG
 808   ArgTrpMe tAlaTrpGlu CysIleLeuM etGlyLysPh eThrThrAla

2551 AGTGACGTGT GGGCCTTTGG TGTGACCCTG TGGGAGGTGC TGATGCTCTG
 824 SerAspValT rpAlaPheGl yValThrLeu TrpGluValL euMetLeuCys

2601 TAGGGCCCAG CCCTTTGGGC AGCTCACCGA CGAGCAGGTC ATCGAGAACG
 841  ArgAlaGln ProPheGlyG lnLeuThrAs pGluGlnVal IleGluAsnAla
```

FIGURE 2-4

```
2651 CGGGGGAGTT CTTCCGGGAC CAGGGCCGGC AGGTGTACCT GTCCCGGCCG
 858   GlyGluPh ePheArgAsp GlnGlyArgG lnValTyrLe uSerArgPro

2701 CCTGCCTGCC CGCAGGGCCT ATATGAGCTG ATGCTTCGGT GCTGGAGCCG
 874 ProAlaCysP roGlnGlyLe uTyrGluLeu MetLeuArgC ysTrpSerArg

2751 GGAGTCTGAG CAGCGACCAC CCTTTTCCCA GCTGCATCGG TTCCTGGCAG
 891  GluSerGlu GlnArgProP roPheSerGl nLeuHisArg PheLeuAlaGlu
                                                    >>>

2801 AGGATGCACT CAACACGGTG TGAATCACAC ATCCAGCTGC CCCTCCCTCA
 908   AspAlaLe uAsnThrVal

2851 GGGAGTGATC CAGGGGAAGC CAGTGACACT AAAACAAGAG GACACAATGG

2901 CACCTCTGCC CTTCCCCTCC CGACAGCCCA TCACCTCTAA TAGAGGCAGT

2951 GAGACTGCAG AAGCCCCTGT CGCCCACCCA GCTGGTCCTG TGGATGGGAT

3001 CCTCTCCACC CTCCTCTAGC CATCCCTTGG GGAAGGGTGG GGAGAAATAT

3051 AGGATAGACA CTGGACATGG CCCATTGGAG CACCTGGGCC CCACTGGACA

3101 ACACTGATTC CTGGAGAGGT GGCTGCGCCC CCAGCTTCTC TCTCCCTGTC

3151 ACACACTGGA CCCCACTGGC TGAGAATCTG GGGGTGAGGA GGACAAGAAG

3201 GAGAGGAAAA TGTTTCCTTG TGCCTGCTCC TGTACTTGTC CTCAGCTTGG

3251 GCTTCTTCCT CCTCCATCAC CTGAAACACT GGACCTGGGG GTAGCCCCGC

3301 CCCAGCCCTC AGTCACCCCC ACTTCCCACC TGCAGTCTTG TAGCTAGAAC

3351 TTCTCTAAGC CTATACGTTT CTGTGGAGTA AATATTGGGA TTGGGGGGAA

3401 AGAGGGAGCA ACGGCCCATA GCCTTGGGGT TGGACATCTC TAGTGTAGCT

3451 GCCACATTGA TTTTTCTATA ATCACTTGGG GTTTGTACAT TTTTGGGGGG

3501 AGAGACACAG ATTTTTACAC TAATATATGG ACCTAGCTTG AGGCAATTTT

3551 AATCCCCTGC ACTAGGCAGG TAATAATAAA GGTTGAGTTT TCCACAAAAA

3601 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA
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FIGURE 3

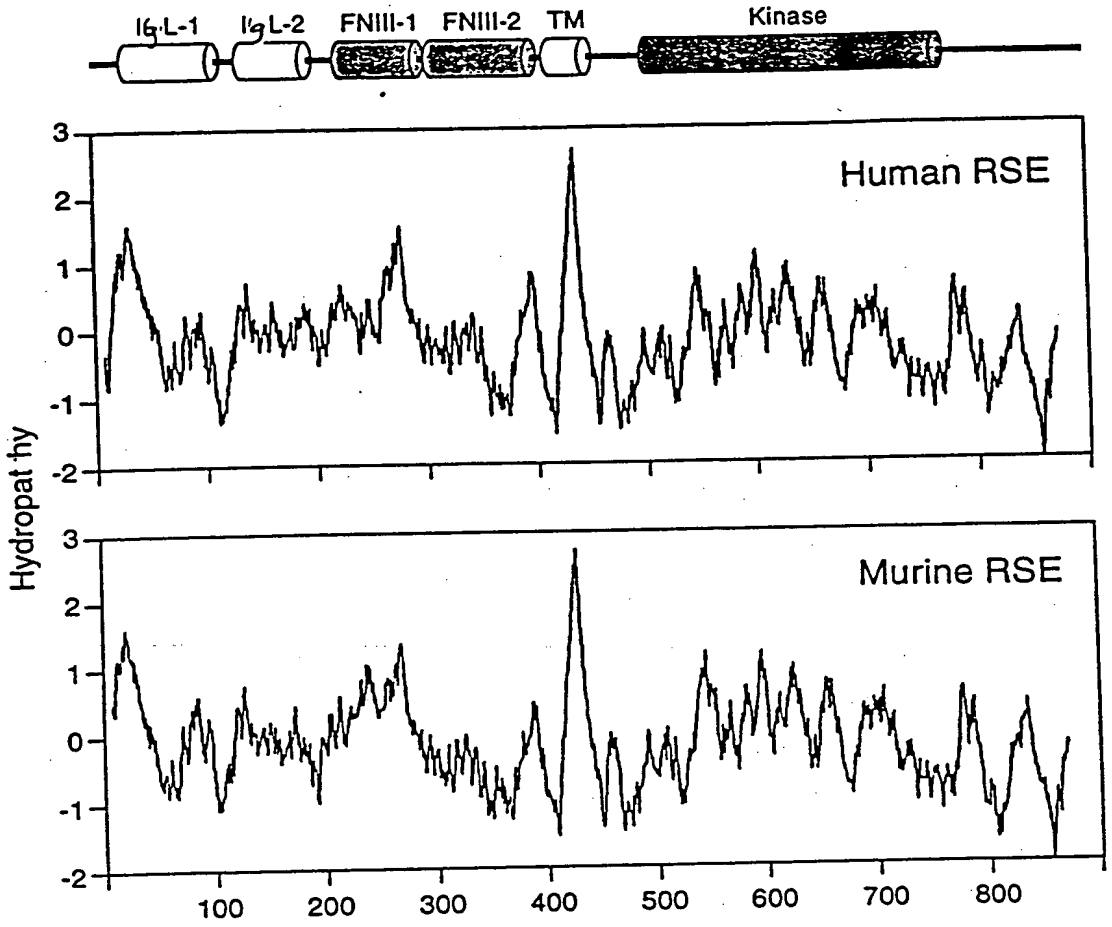
Ig-L-1
Ig-L-2
FNIII-1
FNIII-2
TM
Kinase
Human RSE
Murine RSE
Hydropathy
3
2
1
0
-1
-2
100
200
300
400
500
600
700
800

FIGURE 4-1

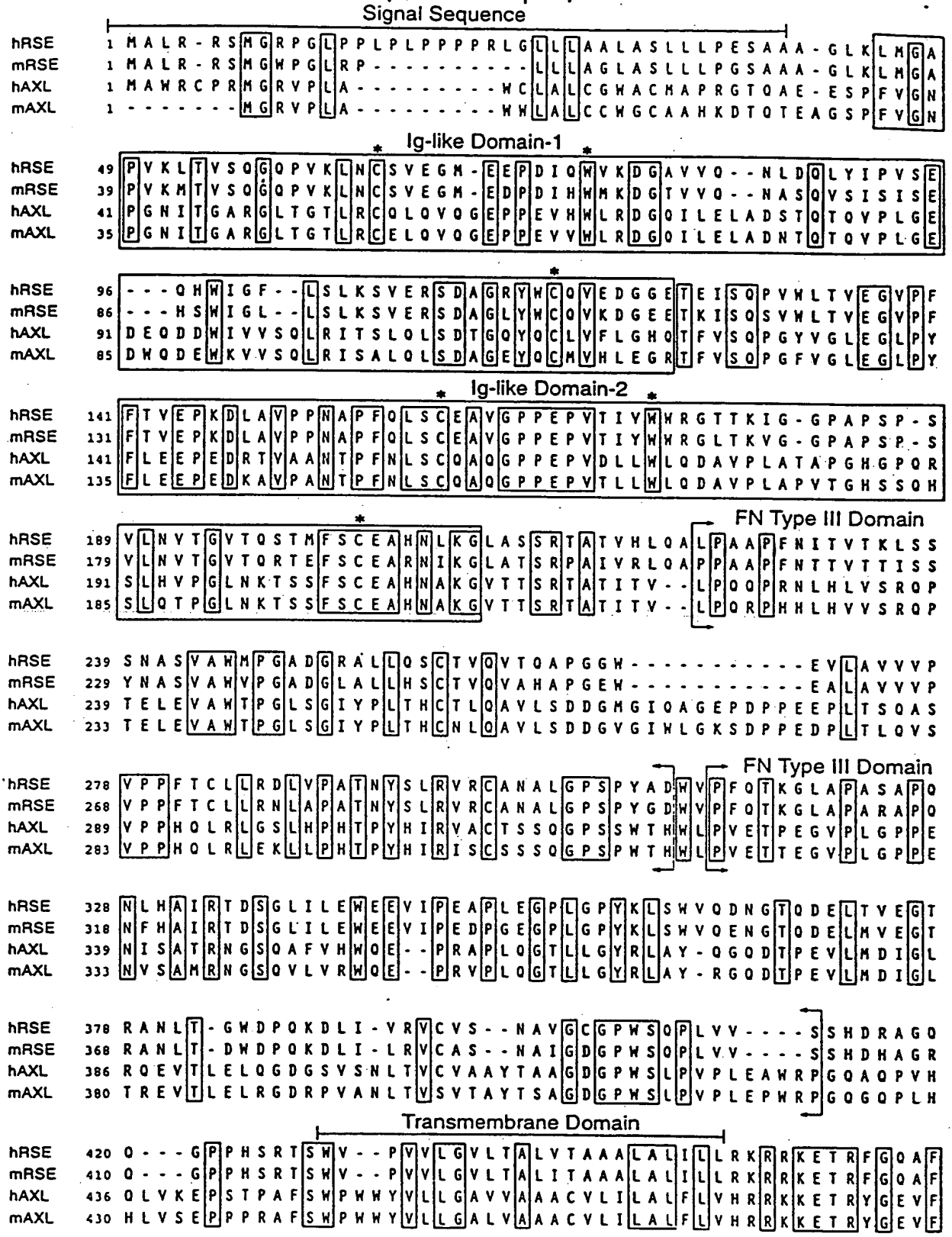
Signal Sequence
Ig-like Domain-1
Ig-like Domain-2
FN Type III Domain
FN Type III Domain
Transmembrane Domain
hRSE
mRSE
hAXL
mAXL

FIGURE 4-2

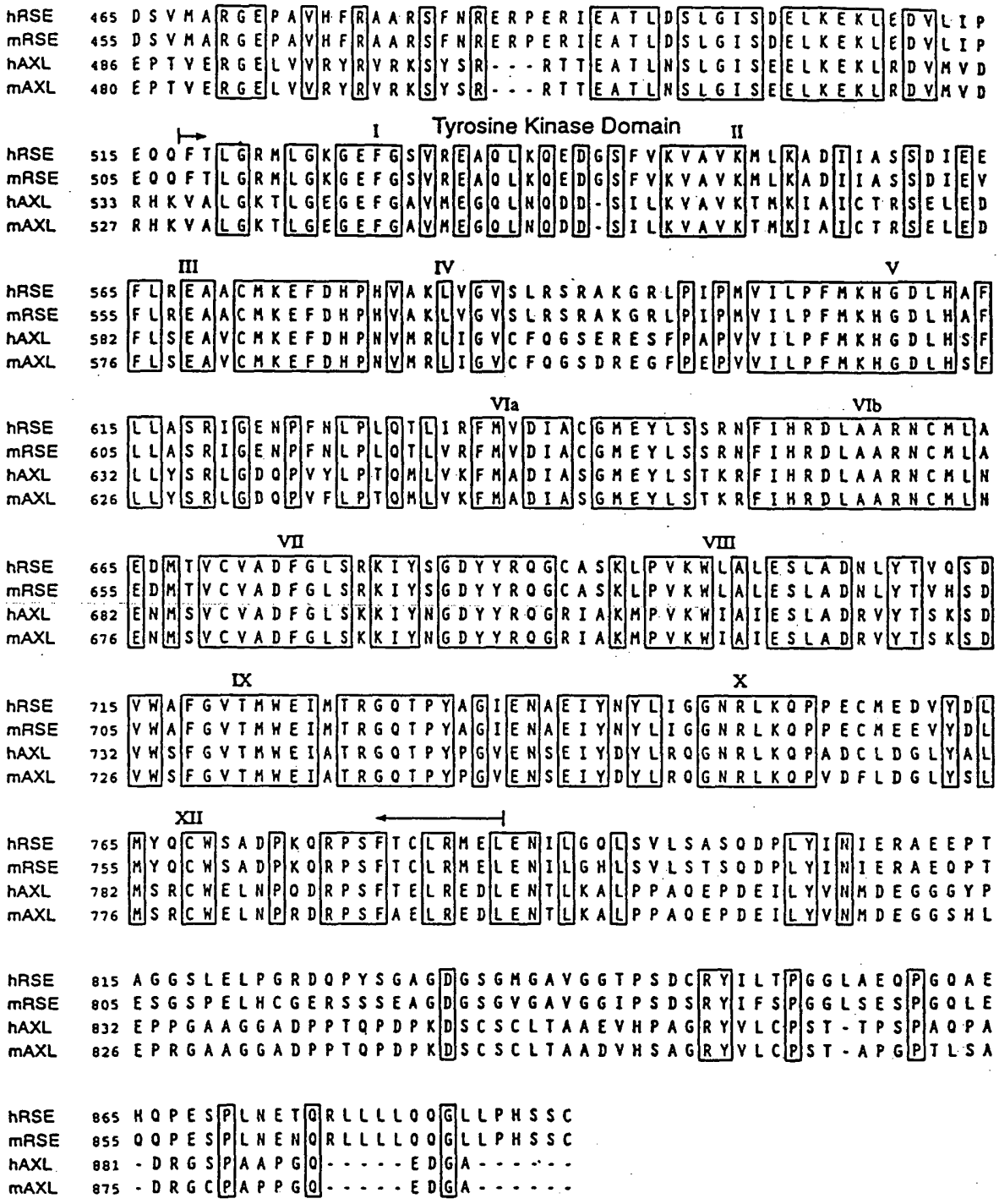
Tyrosine Kinase Domain
I
II
III
IV
V
VIa
VIb
VII
VIII
IX
X
XII
hRSE 465 D S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L G I S D E L K E K L E D V L I P
mRSE 455 D S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L G I S D E L K E K L E D V L I P
hAXL 486 E P T V E R G E L V V R Y R V R K S Y S R - - - R T T E A T L N S L G I S E E L K E K L R D V M V D
mAXL 480 E P T V E R G E L V V R Y R V R K S Y S R - - - R T T E A T L N S L G I S E E L K E K L R D V M V D
hRSE 515 E Q Q F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E
mRSE 505 E Q Q F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E V
hAXL 533 R H K V A L G K T L G E G E F G A V M E G Q L N Q D D - S I L K V A V K T M K I A I C T R S E L E D
mAXL 527 R H K V A L G K T L G E G E F G A V M E G Q L N Q D D - S I L K V A V K T M K I A I C T R S E L E D
hRSE 565 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F
mRSE 555 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F
hAXL 582 F L S E A V C M K E F D H P N V M R L I G V C F Q G S E R E S F P A P V V I L P F M K H G D L H S F
mAXL 576 F L S E A V C M K E F D H P N V M R L I G V C F Q G S D R E G F P E P V V I L P F M K H G D L H S F
hRSE 615 L L A S R I G E N P F N L P L Q T L I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A
mRSE 605 L L A S R I G E N P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A
hAXL 632 L L Y S R L G D Q P V Y L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N
mAXL 626 L L Y S R L G D Q P V F L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N
hRSE 665 E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K W L A L E S L A D N L Y T V Q S D
mRSE 655 E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K W L A L E S L A D N L Y T V H S D
hAXL 682 E N M S V C V A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K W I A I E S L A D R V Y T S K S D
mAXL 676 E N M S V C V A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K W I A I E S L A D R V Y T S K S D
hRSE 715 V W A F G V T M W E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K Q P P E C M E D V Y D L
mRSE 705 V W A F G V T M W E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K Q P P E C M E E V Y D L
hAXL 732 V W S F G V T M W E I A T R G Q T P Y P G V E N S E I Y D Y L R Q G N R L K Q P A D C L D G L Y A L
mAXL 726 V W S F G V T M W E I A T R G Q T P Y P G V E N S E I Y D Y L R Q G N R L K Q P V D F L D G L Y S L
hRSE 765 M Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A S Q D P L Y I N I E R A E E P T
mRSE 755 M Y Q C W S A D P K Q R P S F T C L R M E L E N I L G H L S V L S T S Q D P L Y I N I E R A E Q P T
hAXL 782 M S R C W E L N P Q D R P S F T E L R E D L E N T L K A L P P A Q E P D E I L Y V N M D E G G G Y P
mAXL 776 M S R C W E L N P R D R P S F A E L R E D L E N T L K A L P P A Q E P D E I L Y V N M D E G G S H L
hRSE 815 A G G S L E L P G R D Q P Y S G A G D G S G M G A V G G T P S D C R Y I L T P G G L A E Q P G Q A E
mRSE 805 E S G S P E L H C G E R S S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S E S P G Q L E
hAXL 832 E P P G A A G G A D P P T Q P D P K D S C S C L T A A E V H P A G R Y V L C P S T - T P S P A Q P A
mAXL 826 E P R G A A G G A D P P T Q P D P K D S C S C L T A A D V H S A G R Y V L C P S T - A P G P T L S A
hRSE 865 H Q P E S P L N E T Q R L L L L Q Q G L L P H S S C
mRSE 855 Q Q P E S P L N E N Q R L L L L Q Q G L L P H S S C
hAXL 881 - D R G S P A A P G Q - - - - - E D G A - - - - - -
mAXL 875 - D R G C P A P P G Q - - - - - E D G A - - - - - -

FIGURE 5

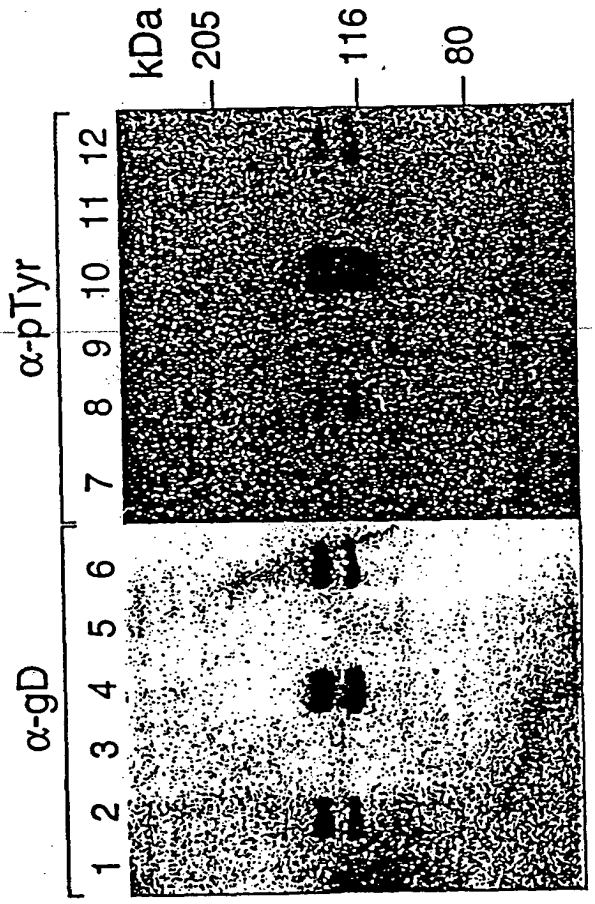

FIGURE 6

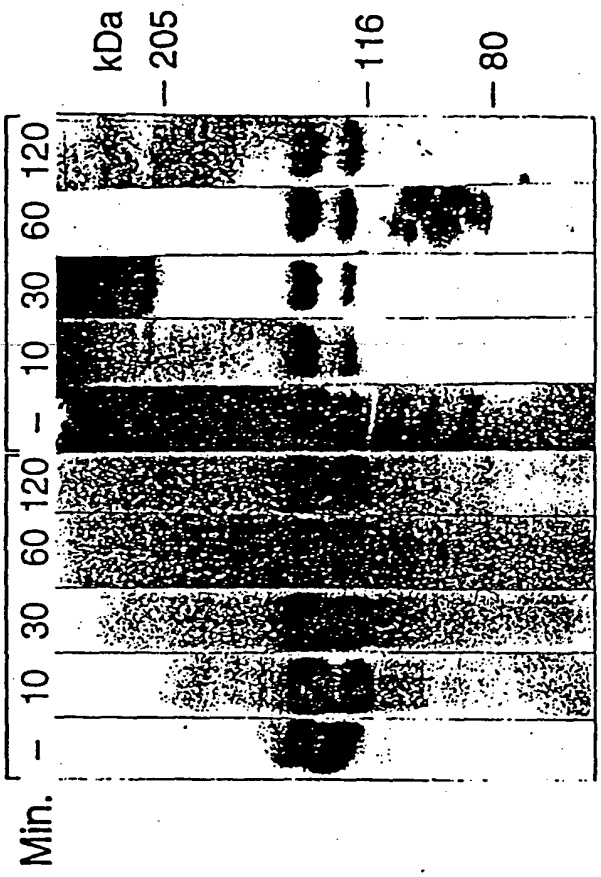

FIGURE 7A

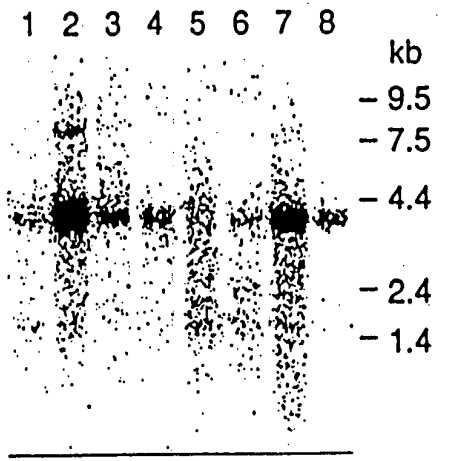

FIGURE 7B

FIGURE 8A

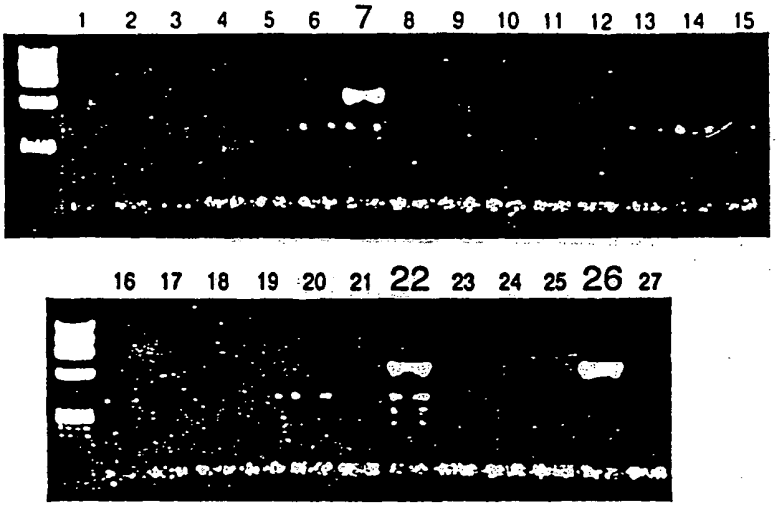

FIGURE 8B

CHROMOSOME CONTENT OF SOMATIC CELL HYBRID PANEL

LANE #	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
CELL LINE	212	324	423	507	683	734	750	756	803	811	852	860	862	867	904	909	937	940	967	968	983	1006	1049	1079	1099
Human Chromosome 1														•			•								•
2											•														
3			•	•								•												•	
4									•													•			
5	•			•	•	•	•	•	•			•	•	•	•	•	•	•	•	•	•	•	•	•	•
6								•				•			•	•									
7								•														•			
8									•	•						•			•			•			
9						•								•						•					
10												•									•				
11									•														•		
12				•	•			•							•										
13							•	•						•						•	•	•			•
14				•	•		•	•						•		•	•								
15																									
16															•					•					
17										•							•							•	
18		•				•				•				•											
19					•		•	•				•		•								•			
20				•				•										•							
21					•			•				•			•		•								
22				•	•				•							•									•
X									•							•					•				
Y	•			•			•								•										

FIGURE 9.

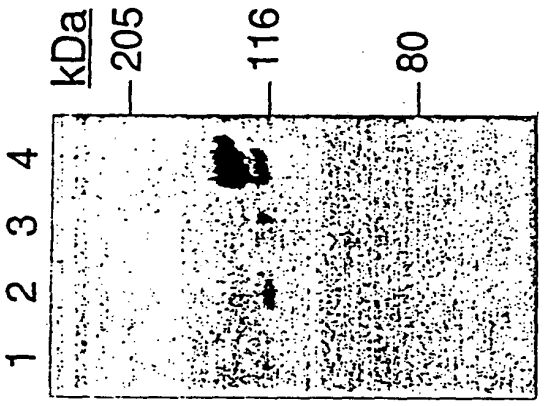

FIGURE 10A.

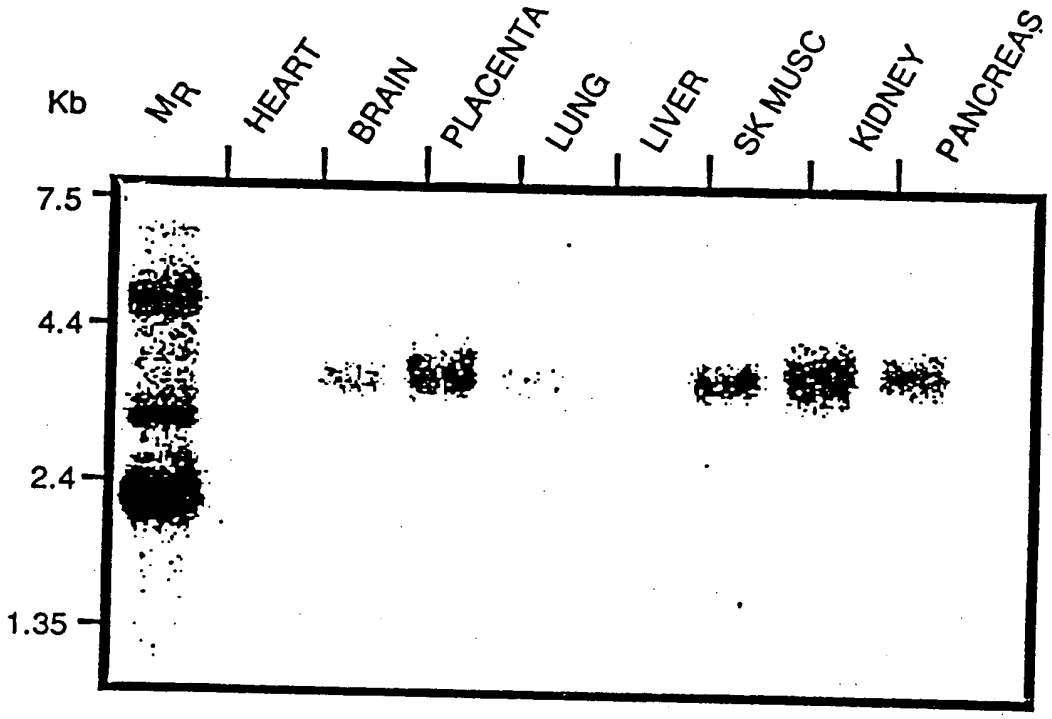

FIGURE 10 B.

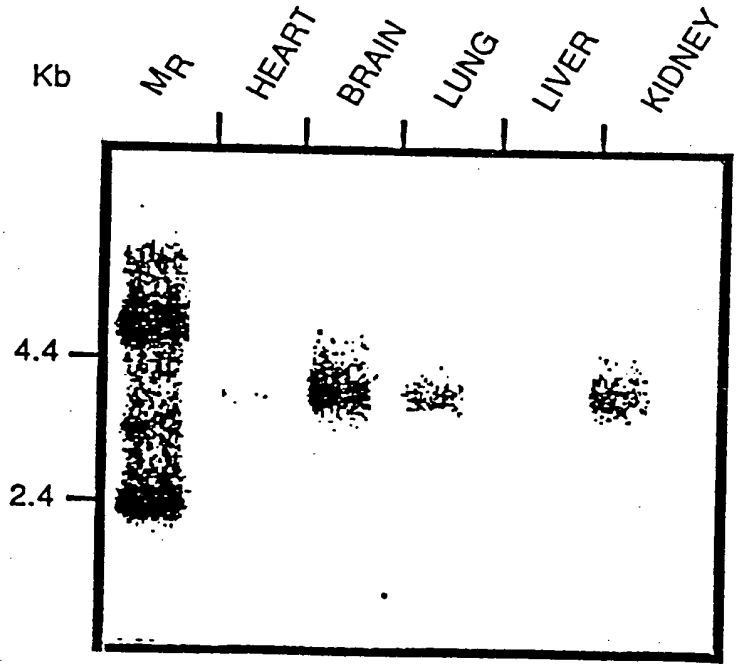

FIGURE 11A

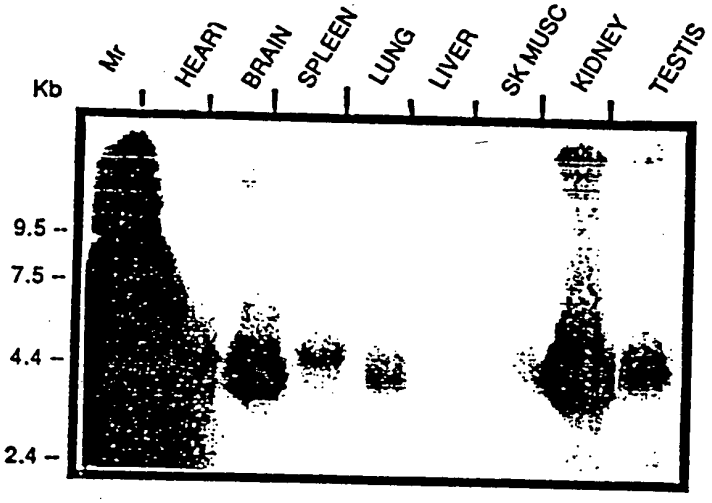

FIGURE 11B

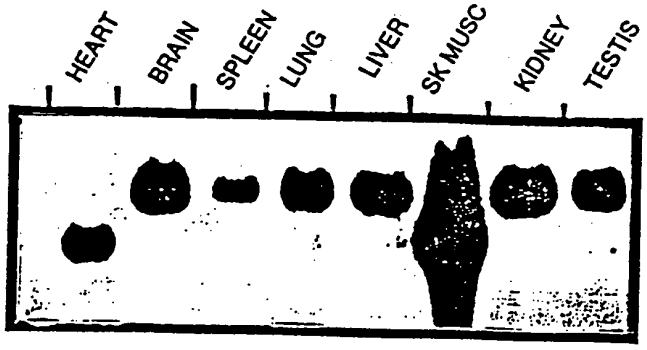

FIGURE 12A

HUMAN -ve STRAND

FIGURE 12B

MOUSE -ve STRAND

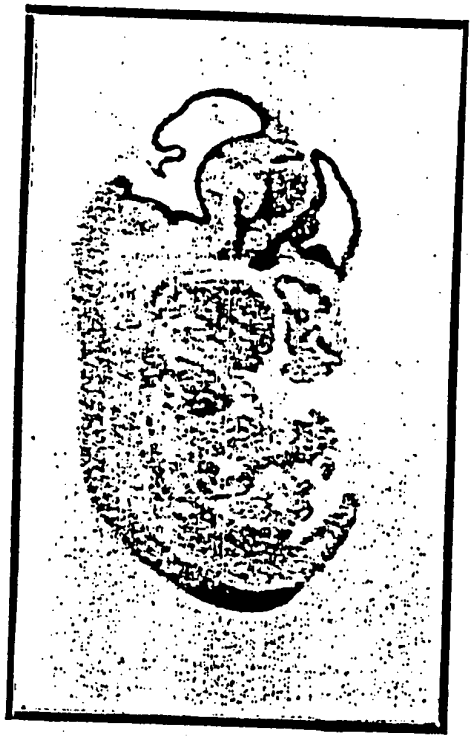

FIGURE 12C

MOUSE +ve STRAND